

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/551,300A  
Source: IFwp  
Date Processed by STIC: 2/10/07

# ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 02/10/2007  
 PATENT APPLICATION: US/10/551,300A TIME: 09:28:04

Input Set : E:\substitute seqlisting 10589-034.TXT  
 Output Set: N:\CRF4\02102007\J551300A.raw

4 <110> APPLICANT: Trotta, Christopher R.  
 6 <120> TITLE OF INVENTION: TARGETING ENZYMES OF THE tRNA SPLICING  
 7 PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR  
 8 ANTI-PROLIFERATIVE MOLECULES  
 10 <130> FILE REFERENCE: 10589-034-999  
 12 <140> CURRENT APPLICATION NUMBER: US/10/551,300A  
 13 <141> CURRENT FILING DATE: 2005-09-27  
 15 <150> PRIOR APPLICATION NUMBER: PCT/US2004/009590  
 16 <151> PRIOR FILING DATE: 2004-03-26  
 18 <150> PRIOR APPLICATION NUMBER: 60/458,067  
 19 <151> PRIOR FILING DATE: 2003-03-27  
 21 <160> NUMBER OF SEQ ID NOS: 4  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 465  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: HsSen2p  
 33 <400> SEQUENCE: 1  
 34 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr  
 35 1 5 10 15  
 36 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly  
 37 20 25 30  
 38 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn  
 39 35 40 45  
 40 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly  
 41 50 55 60  
 42 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile  
 43 65 70 75 80  
 44 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met  
 45 85 90 95  
 46 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala  
 47 100 105 110  
 48 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile  
 49 115 120 125  
 50 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn  
 51 130 135 140  
 52 Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn  
 53 145 150 155 160  
 54 Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp  
 55 165 170 175  
 56 Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys

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57 180 185 190  
 58 Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys  
 59 195 200 205  
 60 Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys  
 61 210 215 220  
 62 Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser  
 63 225 230 235 240  
 64 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu  
 65 245 250 255  
 66 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala  
 67 260 265 270  
 68 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg  
 69 275 280 285  
 70 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala  
 71 290 295 300  
 72 Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys  
 73 305 310 315 320  
 74 Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln  
 75 325 330 335  
 76 Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys  
 77 340 345 350  
 78 Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu  
 79 355 360 365  
 80 Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile  
 81 370 375 380  
 82 Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser  
 83 385 390 395 400  
 84 Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys  
 85 405 410 415  
 86 Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys  
 87 420 425 430  
 88 Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val  
 89 435 440 445  
 90 Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp  
 91 450 455 460  
 92 Leu  
 93 465  
 96 <210> SEQ ID NO: 2  
 97 <211> LENGTH: 448  
 98 <212> TYPE: PRT  
 99 <213> ORGANISM: Homo sapiens  
 101 <220> FEATURE:  
 102 <223> OTHER INFORMATION: HsSen2 variant  
 104 <400> SEQUENCE: 2  
 105 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr  
 106 1 5 10 15  
 107 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly  
 108 20 25 30  
 109 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn

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110	35	40	45	
111	Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly			
112	50	55	60	
113	Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile			
114	65	70	75	80
115	Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met			
116	85	90	95	
117	Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala			
118	100	105	110	
119	Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile			
120	115	120	125	
121	Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn			
122	130	135	140	
123	Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn			
124	145	150	155	160
125	Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp			
126	165	170	175	
127	Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys			
128	180	185	190	
129	Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys			
130	195	200	205	
131	Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys			
132	210	215	220	
133	Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser			
134	225	230	235	240
135	Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu			
136	245	250	255	
137	Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala			
138	260	265	270	
139	Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg			
140	275	280	285	
141	Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu			
142	290	295	300	
143	Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln Pro			
144	305	310	315	320
145	Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys Gly			
146	325	330	335	
147	Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Tyr			
148	340	345	350	
149	Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile Glu			
150	355	360	365	
151	Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser Trp			
152	370	375	380	
153	Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys Glu			
154	385	390	395	400
155	Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys Glu			
156	405	410	415	
157	Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val Ile			
158	420	425	430	

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159 Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp Leu  
 160 435 440 445  
 163 <210> SEQ ID NO: 3  
 164 <211> LENGTH: 377  
 165 <212> TYPE: PRT  
 166 <213> ORGANISM: *Saccharomyces cerevisiae*  
 168 <220> FEATURE:  
 169 <223> OTHER INFORMATION: Sc Sen2p  
 171 <400> SEQUENCE: 3  
 172 Met Ser Lys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro  
 173 1 5 10 15  
 174 Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu  
 175 20 25 30  
 176 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu  
 177 35 40 45  
 178 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile  
 179 50 55 60  
 180 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe  
 181 65 70 75 80  
 182 Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg  
 183 85 90 95  
 184 Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly  
 185 100 105 110  
 186 Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr  
 187 115 120 125  
 188 Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys  
 189 130 135 140  
 190 Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp  
 191 145 150 155 160  
 192 Glu Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe  
 193 165 170 175  
 194 Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Asp  
 195 180 185 190  
 196 Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu  
 197 195 200 205  
 198 Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Leu Met Pro Val Glu  
 199 210 215 220  
 200 Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala  
 201 225 230 235 240  
 202 Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile  
 203 245 250 255  
 204 His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His  
 205 260 265 270  
 206 Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu  
 207 275 280 285  
 208 Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly  
 209 290 295 300  
 210 Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala  
 211 305 310 315 320

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212 Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu  
213 325 330 335  
214 Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn  
215 340 345 350  
216 Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys  
217 355 360 365  
218 Arg Trp Val Pro Gly Arg Asn Arg Asp  
219 370 375  
222 <210> SEQ ID NO: 4  
223 <211> LENGTH: 5  
224 <212> TYPE: PRT  
225 <213> ORGANISM: Artificial Sequence  
227 <220> FEATURE:  
228 <223> OTHER INFORMATION: Motif of the active site for the 5' splice site of yeast  
229 and archaeal tRNA splicing endonuclease  
231 <400> SEQUENCE: 4  
232 Tyr Arg Gly Gly Tyr  
233 1 5

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/551,300A

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Input Set : E:\substitute seqlisting 10589-034.TXT

Output Set: N:\CRF4\02102007\J551300A.raw